

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lal, Preeti
 Shah, Purvi
 Corley, Neil C.

(ii) TITLE OF THE INVENTION: HUMAN MEMBRANE RECYCLING PROTEINS

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 (B) STREET: 3174 Porter Dr.
 (C) CITY: Palo Alto
 (D) STATE: CA
 (E) COUNTRY: USA
 (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM Compatible
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
 (B) FILING DATE: Filed Herewith
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/360,125
 (B) FILING DATE: July 23, 1999

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/004,502
 (B) FILING DATE: January 8, 1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
 (B) REGISTRATION NUMBER: 36,749
 (C) REFERENCE/DOCKET NUMBER: PF-0456 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
 (B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: TONGTUT01
 (B) CLONE: 980615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Gln Ser Arg Asp Gly Gly Asn Pro Phe Ala Glu Pro Ser Glu
 1 5 10 15
 Leu Asp Asn Pro Phe Gln Asp Pro Ala Val Ile Gln His Arg Pro Ser

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(vi) IMMEDIATE SOURCE:

- (A) LIBRARY: TONGTUT01
(B) CLONE: 980615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

NGACGCAGG	GCAACCCACG	GCTGCTCGGG	GGATCCTGT	GGCCCTTCCG	GTCGATGGAA	60
CCAATCCGTG	CACAGAGAAG	CGGGGGCAGAC	TGAGGGCGAGT	GAAGTGGACT	CTGAGGGCTA	120
CCGCTACCAGC	CACTGCTGCG	GCAGGGGCGT	GGAGGGCAGA	GGGCCGCGGA	GGCCGCAGTT	180
GCAAACATGG	CTCAGAGCAG	AGACGGCGGA	AACCCGTTGCG	CCGAGCCCAG	CGAGCTTGAC	240
AACCCCTTTC	AGGACCCAGC	TGTGATCCAG	CACCGACCCA	GCCGGCAGTA	TGCCACGTT	300
GACGTCTACA	ACCCTTTGTA	GACCCGGGAG	CCACCAACAG	CCTATGAGCC	TCCAGCCCCCT	360
GCCCCATTGC	CTCCACCCCTC	AGCTCCCTCC	TTGCAGCCCT	CGAGAAAGCT	CAGCCCCACA	420
GAACCTAAGA	ACTATGGCTC	ATACAGCACT	CAGGCCTCAG	CTGCAGCAGC	CACAGCTGAG	480
CTGCTGAAGA	AACAGGAGGA	GCTCAACCGG	AAGGCAGAGG	AGTTGGACCC	AAGGGAGCGA	540
GAGCTGCAGC	ATGCTGCCCT	GGGGGGCACA	GCTACTCGAC	AGAACAAATTG	GCCCCCTCTA	600
CCTTCTTTT	GTCCAGTTCA	GCCCTGCTT	TTCCAGGACA	TCTCCATGGA	GATCCCCCAA	660

GAATTTCA	AGACTGTATC	CACCATGTAC	TACCTCTGGA	TGTGCAGCAC	GCTGGCTCTT	720
CTCCTGA	ACT TCCCTCG	CCTGGCCAGC	TTCTGTGTTG	AAACCAACAA	TGGCGCAGGC	780
TTTGGGCT	TTT CTATCCTCTG	GGTCCTCCTT	TTCACTCCCT	GCTCCTTG	CTGCTGGTAC	840
CGCCCCATG	ATAAGGCTT	CCGGAGTGC	AGTTCAATTCA	ATTTCCTCGT	TTTCTTCTTC	900
ATTTTCTCG	TCCAGGATGT	GCTCTTGTC	CTCCAGGCCA	TTGGTATCCC	AGGTTGGGA	960
TTCAGTGGC	GGATCTCTGC	TCTGGTGGTG	CCGAAGGGCA	ACACAGCAGT	ATCCGTGCTC	1020
ATGCTGCTG	TCGCCCTGCT	CTTCACTGGC	ATTGCTGTG	TAGGAATTGT	CATGCTGAAA	1080
CGGATCCACT	CCTTATACCG	CCGCACAGGT	GCCAGCTTTC	AGAAGGCCA	GCAAGAATT	1140
GCTGCTGGT	TCTTCTCAA	CCCTGCGGTG	CGAACCGCAG	CTGCCAATGC	AGCCGCTGGG	1200
GCTGCTGAA	ATGCCTCCG	GGCCCCGTGA	CCCCTGACTG	GGATGCCCTG	GCCCTGCTAC	1260
TTGAGGGAGC	TGACTTAGCT	CCCCTCCCTA	AGGTCTCTGG	GACTTGGAGA	GACATCACTA	1320
ACTGATGGCT	CCTCCGTAGT	GCTCCAATC	CTATGGCCAT	GACTGCTGAA	CCTGACAGGC	1380
GTGTGGGGAG	TTCACTGTGA	CCTAGTCCCC	CCATCAGGCC	ACACTGCTGC	CACCTCTCAC	1440
ACGCCCCAAC	CCAGCTTCCC	TCTGCTGTG	CACGGCTGTT	GCTTCGGTTA	TTTAAATAAA	1500
AAGAAAGTGG	AACTGGA	ACT G				1521

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT01
- (B) CLONE: 412453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Ala	Phe	Asp	Thr	Asn	Pro	Phe	Ala	Asp	Pro	Val	Asp	Val	Asn
1			5					10				15			
Pro	Phe	Gln	Asp	Pro	Ser	Val	Thr	Gln	Leu	Thr	Asn	Ala	Pro	Gln	Gly
							20		25			30			
Gly	Leu	Ala	Glu	Phe	Asn	Pro	Phe	Ser	Glu	Thr	Asn	Ala	Ala	Thr	Thr
							35		40			45			
Val	Pro	Val	Thr	Gln	Leu	Pro	Gly	Ser	Ser	Gln	Pro	Ala	Val	Leu	Gln
							50		55			60			
Pro	Ser	Val	Glu	Pro	Thr	Gln	Pro	Thr	Pro	Gln	Ala	Val	Val	Ser	Ala
							65		70			75			80
Ala	Gln	Ala	Gly	Leu	Leu	Arg	Gln	Gln	Glu	Glu	Leu	Asp	Arg	Lys	Ala
							85		90			95			
Ala	Glu	Leu	Glu	Arg	Lys	Glu	Arg	Glu	Leu	Gln	Asn	Thr	Val	Ala	Asn
							100		105			110			
Leu	His	Val	Arg	Gln	Asn	Asn	Trp	Pro	Pro	Leu	Pro	Ser	Trp	Cys	Pro
							115		120			125			
Val	Lys	Pro	Cys	Phe	Tyr	Gln	Asp	Phe	Ser	Thr	Glu	Ile	Pro	Ala	Asp
							130		135			140			
Tyr	Gln	Arg	Ile	Cys	Lys	Met	Leu	Tyr	Tyr	Leu	Trp	Met	Leu	His	Ser
							145		150			155			160
Val	Thr	Leu	Phe	Leu	Asn	Leu	Ala	Cys	Leu	Ala	Trp	Phe	Ser	Gly	
							165		170			175			
Asn	Ser	Ser	Lys	Gly	Val	Asp	Phe	Gly	Leu	Ser	Ile	Leu	Trp	Phe	Leu
							180		185			190			
Ile	Phe	Thr	Pro	Cys	Ala	Phe	Leu	Cys	Trp	Tyr	Arg	Pro	Ile	Tyr	Lys
							195		200			205			
Ala	Phe	Arg	Ser	Asp	Asn	Ser	Phe	Ser	Phe	Phe	Val	Phe	Phe	Phe	Val
							210		215			220			
Phe	Phe	Cys	Gln	Ile	Gly	Ile	Tyr	Ile	Ile	Gln	Leu	Val	Gly	Ile	Pro
							225		230			235			240
Gly	Leu	Gly	Asp	Ser	Gly	Trp	Ile	Ala	Ala	Leu	Ser	Thr	Leu	Asp	Asn
							245		250			255			
His	Ser	Leu	Ala	Ile	Ser	Val	Ile	Met	Met	Val	Val	Ala	Gly	Phe	Phe
							260		265			270			
Thr	Leu	Cys	Ala	Val	Leu	Ser	Val	Phe	Leu	Leu	Gln	Arg	Val	His	Ser
							275		280			285			
Leu	Tyr	Arg	Arg	Thr	Gly	Ala	Ser	Phe	Gln	Gln	Ala	Gln	Glu	Glu	Phe

290	295	300
Ser Gln Gly Ile Phe Ser	Ser Arg Thr Phe His	Arg Ala Ala Ser Ser
305	310	315
Ala Ala Gln Gly Ala Phe Gln Gly Asn		320
	325	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT01
- (B) CLONE: 412453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

NCCGGAAGTG	GAGGGTCTAC	ACGAAGCGCC	GCTGGGTCTG	GGTGCCCGGA	GGCAGCAGCG	60
TTCGCGGAGT	TCGCCCCGCTG	GCCCCCGATC	ACCATGTCGG	CTTCGACAC	CAACCCCTTC	120
GCGGACCCAG	TGGATGTAAA	CCCCTTCCAG	GATCCCTCTG	TGACCCAGCT	GACCAACGCC	180
CCGCAGGGCG	GCCTGGCGGA	ATTCAACCCC	TTCTCAGAGA	CAAATGCAGC	GACAACAGTT	240
CCTGTACACC	AACTCCCTGG	GTCCTCACAG	CCAGCGGTC	TCCAGGCCATC	AGTGGAACCA	300
ACCCAGCCGA	CCCCCCAGGC	CGTGGTGTCT	GCAGGCCAGG	CAGGCCCTGCT	CCGGCAGCAG	360
GAAGAACTGG	ACAGGAAAGC	TGCCGAGCTG	GAACGCAAGG	AGCAGGGAGCT	GCAGAACACT	420
GTAGCCAAC	TGCATGTGAG	ACAGAACAAAC	TGGCCCCCTC	TGCCCTCGTG	GTGCCCTGTG	480
AAGCCCTGCT	TCTATCAGGA	TTTCTCCACA	GAGATCCCTG	CCGACTACCA	GCGGATATGC	540
AAGATGCTCT	ACTATCTGTG	GATGTTGCAT	TCAGTGACTC	TGTTTCTGAA	CCTGCTTGCC	600
TGCCTGGCCT	GGTTCTCGGG	CAACAGCTCC	AAGGGAGTGG	ACTTTGGCCT	CTCCATCCTG	660
TGGTTTCTGA	TCTTCACTCC	CTGTGCCCTC	CTTGTGTTGGT	ACCGACCCAT	CTATAAGGCC	720
TTTAGGTCCTG	ACAACCTCTT	CAGCTTCTTT	GTGTTCTTCT	TTGTATTTTT	TTGTCAAATA	780
GGGATCTACA	TCATCCAGTT	GGTTGGCATH	CCTGGCCTGG	GGGACAGCGG	TTGGATTGCA	840
GCCCTGTCTA	CACTGGATAA	TCATTCCCTG	GCCATATCAG	TCATCATGAT	GGTGGTGGCT	900
GGCTTCTCTA	CCCTCTGTGC	CGTGCTCTCA	GTCTTCTCTC	TGCAGCGGGT	GCACTCCCTC	960
TACCGACGGA	CAGGGGCCAG	CTTCCAGCAG	CCCCAGGAGG	AGTTTCCCAC	GGGCATCTTC	1020
AGCAGCAGAA	CCTTCCACAG	AGCTGCTTC	TCTGCTGCC	AAGGAGCCCT	CCAGGGGAAT	1080
TAGTCCTCT	CTCTTCTCTC	CCCCTCAGCC	TCTCTCTCGC	CTGCCTTCTG	AGCTGCACTT	1140
TCCGTGGGTG	CCTTATGTGG	TGGTGGTTGT	GCCCAGCAC	GACCTGGCAG	GGTTCTTGCC	1200
GTGGCTCTC	CTCCTCCCTC	AGCGACCAGC	TCTCCCTGGA	ACGGGAGGGA	CAGGGAAATT	1260
TTTCCCCCTC	TATGTACAAA	AAAAAACAAA	GCTCTCTTTC	CTTCTCTGGT	GATGGTTGG	1320
TAGGATTCTT	TTGTCTCTGG	AAGCAGTGGG	ACTGAAGTTC	TCTTCGTCCT	GTGCACACAC	1380
AGACACCCCC	ACACAGTTGG	GATCACAGGC	TGACCTGGGC	CCATCCCAGC	TGGAGCTTTC	1440
TGCCAGGGTC	CTGGGCCTTG	ACTCCCCCAC	CCTGCAGGGC	TGGCCTGAAT	CTGGCTTCTT	1500
AGACACAGCC	CAGTCCTTCC	TGCCTGGCT	GGGAATAAGC	CTCTCACAGG	TTCTGGTGG	1560
CAGATCTGTT	CCCCCAGGTCA	CTCCAGTGGT	CTCCAGGCTT	CCAGAGAAGG	CTGGTTGCCT	1620
CAAGCTCTC	TCTGCCTCAT	AAACGGATCC	AGAGAAGGCT	GGTTGCCTTA	AGCTCTTCCC	1680
TGCCTCGTGT	TCCTGAGAAA	CGGATTAATA	GCCCTTTATC	CCCCTGCACC	CTCCTGCAGG	1740
GGATGGCACT	TTGAGCCCTC	TGGAGCCCTC	CCCTTGCTGA	GCCTTAECTCT	CTTCAGACTT	1800
TCTGAATGTA	CAGTGCCGTT	GGTGGGATT	TGGGGACTGG	AAGGGACCAA	GGACACTGAC	1860
CCCAAGCTGT	CCTGCCTAGC	GTCCAGCGTC	TTCTAGGAGG	GTGGGGTCTG	CCTGCTCTGG	1920
TGTGGTTGGT	TTGGCCCTGT	TTGCTGTGAC	TACCCCCCCC	CCTCCCCGAA	CCGAGGGACG	1980
GCTGCCTTGT	TCTCTGCCTC	AGATGCCACC	TGCCCCGCC	ATGCTCCCCA	TCAGCAGCAT	2040
CCAGACTTTC	AGGAAGGGCA	GGACCAAGCCA	GTCCAGAAC	GCATCCCTCA	GCAGGGACTG	2100
ATAAGCCATC	TCTCGGAGGG	CCCCCTAATA	CCCAGTGGAG	TCTGGTTAC	ACCCCTGGGG	2160
GTGTGTCACT	GTGATGGGAC	ACGTAGGAGT	CCACCCCTAA	AACCAGCACC	CTGTCCCTCG	2220
AGGCTGCCGA	GTGGGTGTGT	GGACTGGGGT	GCCTTCCCAC	AAAACTAGCC	TCCGGCTCTG	2280
GGCCCGAGAC	AGCCGCAGGC	CCCAGCCACT	GAATGATACT	GGCAGCGGGT	GGGGTTTAT	2340
GAACTCCTT	CTGGTATTTT	TTCCCTCTA	TGTACAAATG	TATATGTTAC	GTCTCAATT	2400
TTGTGCTTAA	GTAAAAATAA	AAACATTTC	AGAC			2434

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 487057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ser	Asp	Phe	Asp	Ser	Asn	Pro	Phe	Ala	Asp	Pro	Asp	Leu	Asn	Asn
1								5					10		15
Pro	Phe	Lys	Asp	Pro	Ser	Val	Thr	Gln	Val	Thr	Arg	Asn	Val	Pro	Pro
								20			25		30		
Gly	Leu	Asp	Glu	Tyr	Asn	Pro	Phe	Ser	Asp	Ser	Arg	Thr	Pro	Pro	Pro
								35			40		45		
Gly	Gly	Val	Lys	Met	Pro	Asn	Val	Pro	Asn	Thr	Gln	Pro	Ala	Ile	Met
								50			55		60		
Lys	Pro	Thr	Glu	Glu	His	Pro	Ala	Tyr	Thr	Gln	Ile	Thr	Lys	Glu	His
								65			70		75		80
Ala	Leu	Ala	Gln	Ala	Glu	Leu	Leu	Lys	Arg	Gln	Glu	Glu	Leu	Glu	Arg
								85			90		95		
Lys	Ala	Ala	Glu	Leu	Asp	Arg	Arg	Glu	Arg	Glu	Met	Gln	Asn	Leu	Ser
								100			105		110		
Gln	His	Gly	Arg	Lys	Asn	Asn	Trp	Pro	Pro	Leu	Pro	Ser	Asn	-Phe	Pro
								115			120		125		
Val	Gly	Pro	Cys	Phe	Tyr	Gln	Asp	Phe	Ser	Val	Asp	Ile	Pro	Val	Glu
								130			135		140		
Phe	Gln	Lys	Thr	Val	Lys	Leu	Met	Tyr	Tyr	Leu	Trp	Met	Phe	His	Ala
								145			150		155		160
Val	Thr	Leu	Phe	Leu	Asn	Ile	Phe	Gly	Cys	Leu	Ala	Trp	Phe	Cys	Val
								165			170		175		
Asp	Ser	Ser	Arg	Ala	Val	Asp	Phe	Gly	Leu	Ser	Ile	Leu	Trp	Phe	Leu
								180			185		190		
Leu	Phe	Thr	Pro	Cys	Ser	Phe	Val	Cys	Trp	Tyr	Arg	Pro	Leu	Tyr	Gly
								195			200		205		
Ala	Phe	Arg	Ser	Asp	Ser	Ser	Phe	Arg	Phe	Phe	Val	Phe	Phe	Phe	Val
								210			215		220		
Tyr	Ile	Cys	Gln	Phe	Ala	Val	His	Val	Leu	Gln	Ala	Ala	Gly	Phe	His
								225			230		235		240
Asn	Trp	Gly	Asn	Cys	Gly	Trp	Ile	Ser	Ser	Leu	Thr	Gly	Leu	Asn	Lys
								245			250		255		
Asn	Ile	Pro	Val	Gly	Ile	Met	Met	Ile	Ile	Ile	Ala	Ala	Leu	Phe	Thr
								260			265		270		
Ala	Ser	Ala	Val	Ile	Ser	Leu	Val	Met	Phe	Lys	Lys	Val	His	Gly	Leu
								275			280		285		
Tyr	Arg	Thr	Thr	Gly	Ala	Ser	Phe	Glu	Lys	Ala	Gln	Gln	Glu	Phe	Ala
								290			295		300		
Thr	Gly	Val	Met	Ser	Asn	Lys	Thr	Val	Gln	Thr	Ala	Ala	Ala	Asn	Ala
								305			310		315		320
Ala	Ser	Thr	Ala	Ala	Thr	Ser	Ala	Ala	Gln	Asn	Ala	Phe	Lys	Gly	Asn
								325			330		335		

Gln-Met